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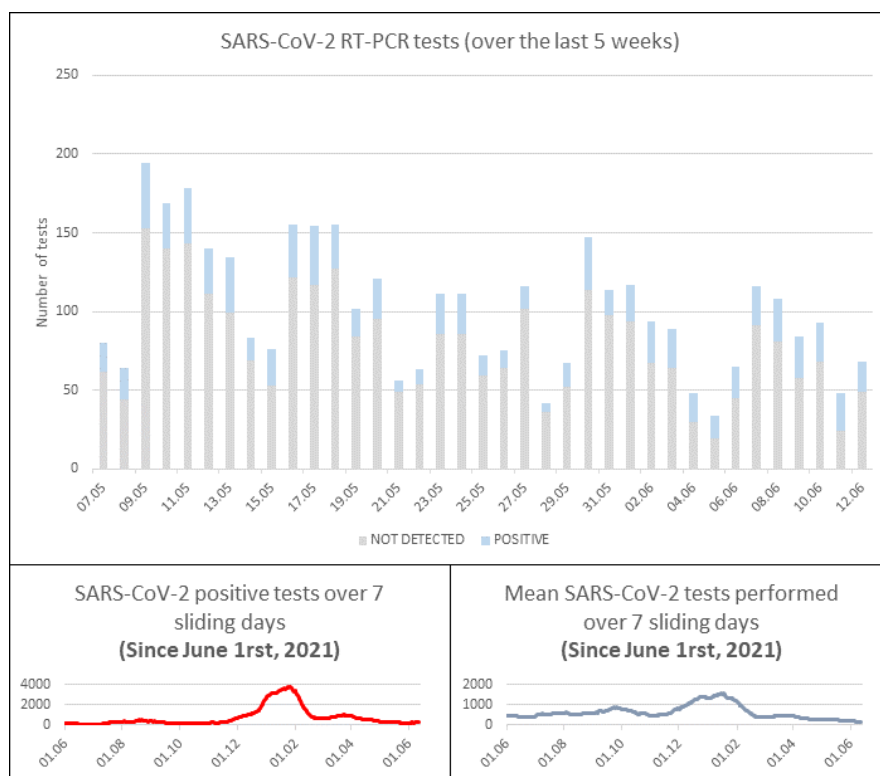
Diagnostic Department

## SARS-CoV-2 genomic surveillance in Geneva: bi-weekly update

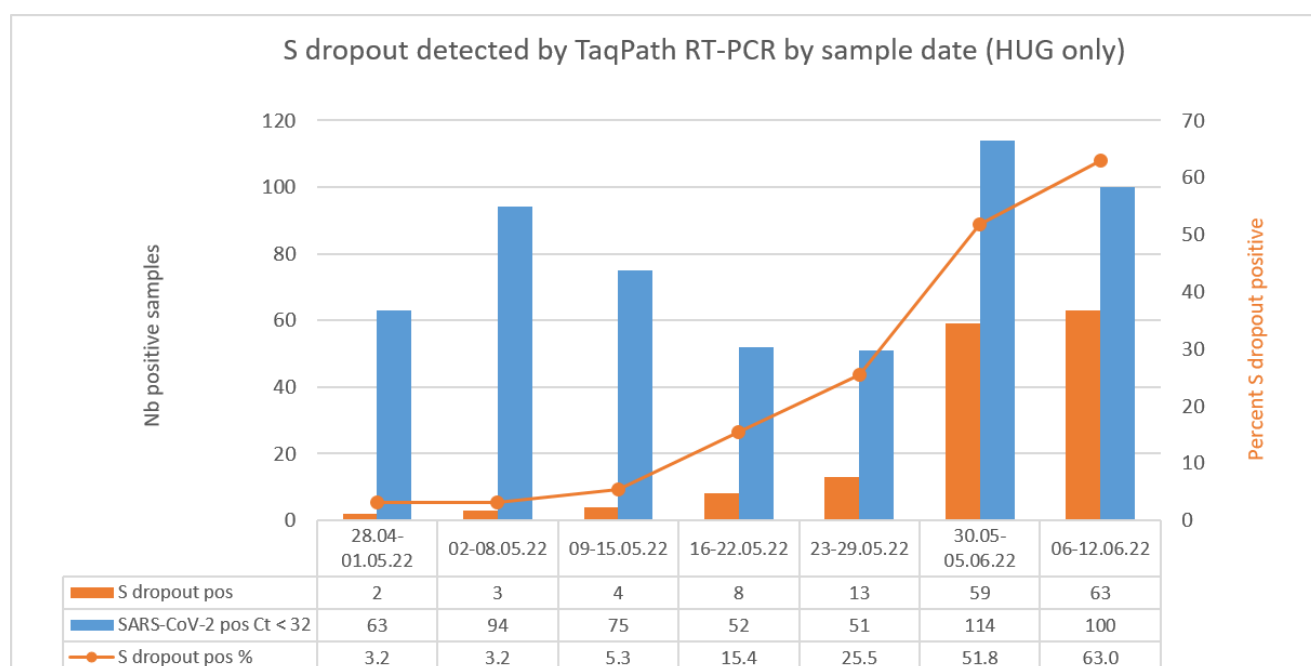
### Highlights:

- While the number of tests performed by our laboratory continues to decline, the absolute number of positive tests and the positivity rate increased over the last 2 weeks to reach again 30% at the end of week 23, indicating that while less people are getting tested, the circulation of the virus started to increase again in the community. (Figure 1).
- **The BA.4/5 Omicron sublineages (assessed by the “S Dropout”) are now dominant in the Geneva area**, as shown in Figure 2. They caused more than 60% of the new infections at the end of week 23.
- **This trend is confirmed by WGS** (Figure 3), which shows the BA.5 dominance.
- Note that Omicron recombinants have not been detected any more during the last 3 weeks (The XM recombinants collected at the end of the month of April were due to a nosocomial cluster).

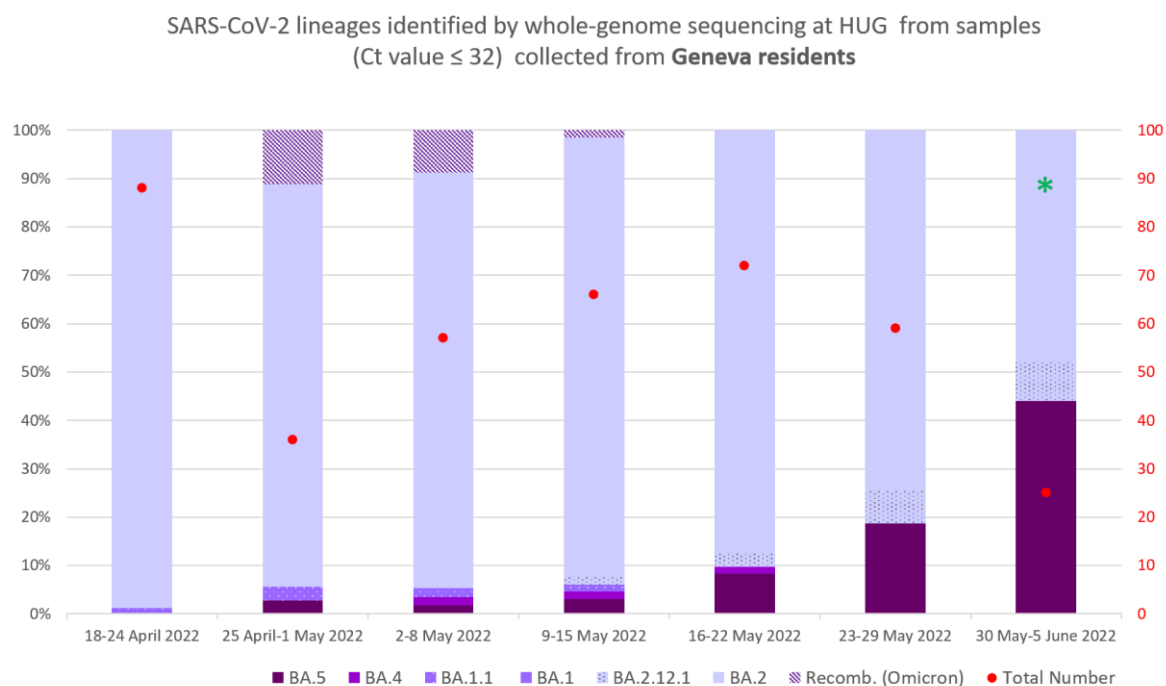
**Figure 1:** Number of SARS-CoV-2 tests performed at the HUG laboratory of virology (per day). Positive tests are displayed in light blue (top). Bottom left: SARS-CoV-2 positive tests over 7 sliding days. Bottom right: mean SARS-CoV-2 tests performed over 7 sliding days.



**Figure 2:** Weekly evolution of the S Drop out among specimens collected at HUG (including both ambulatory and hospitalized patients). All positive samples collected at HUG (both in in- and outpatients) with a Ct value < 32 are tested for the S Drop out.



**Figure 3:** SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value  $\leq 32$ ) collected from Geneva residents (*Sentinella* specimens excluded). \*Sequencing is still ongoing for week 22 (May 30 to June 5, 2022). A total of 403 sequences are included in this analysis.



Laurent Kaiser, Samuel Cordey, Manuel Schibler and Pauline Vetter for HUG.  
 Emma Hodcroft for the Geneva Center for Emerging Viral Diseases.  
 Pauline Brindel for the Geneva Cantonal Physician team.

### **The laboratory of virology of the Geneva University Hospitals as a sentinel site for the Geneva area**

The number of tests (PCR and antigen tests) performed at the Geneva University Hospitals represented around 25% (1120/4519) and 22% (879/3955) of the total number of tests performed in the canton of Geneva during weeks 22 and 23 of 2022, respectively. Roughly 23% and 19% of the positive specimens collected in the Geneva area were processed at HUG during weeks 22 and 23 (201/863 and 200/1029), respectively. Samples collected from symptomatic individuals at our outpatient testing center are tested by RT-PCR. Specimens analyzed in our laboratory originate from ambulatory and hospitalized patients as well as symptomatic and/or asymptomatic health care workers.

The number of positive tests in the canton and the total number of tests done during the surveilled week are available on the website from Federal Office of Public Health ([COVID-19 Suisse | Coronavirus | Dashboard \(admin.ch\)](https://www.admin.ch/gov/de/section/0460/data/04603/COVID-19_Suisse_Coronavirus_Dashboard_admin.ch)). During weeks 22 and 23 in the canton of Geneva, the number of RT-PCR tests continued to decrease. However, the number of confirmed cases significantly increased by 50% over the 2 weeks and the proportion of positive tests was above 30% during week 23.

### **Methods and collaborations**

The laboratory has stopped the screening for the “S Drop out” (Taqpath RT-PCR assay) at the end of week 14 of 2022, after the replacement of BA.1 by BA.2. However, in order to monitor the potential arrival of BA.4/BA.5 variants in the Geneva area, the “S Drop out” analysis has been reintroduced from week 18 on positive samples with Ct values < 32 tested in our laboratory. Until week 20, for any “S Drop out” detected, a screening for the 452R mutation is then carried out; as 100% of the S Drop out positive specimens were carrying the 452R mutation (highly suggestive of BA.4/5), we stopped this additional analysis at the beginning of week 21. Whole genome sequencing (WGS) performed on SARS-CoV-2 positive samples within the Swiss national SARS-CoV-2 genomic and variants surveillance program allows for definitive sublineage/variant identification.

WGS is carried out in close collaboration with the Health 2030 Genome Center in Geneva and Philippe Le Mercier from the Swiss Institute of Bioinformatics. The national genomic surveillance program is ongoing in Switzerland since March 1, 2021 and includes specimens collected at HUG with a Ct-value ≤32. In some instances, sequencing can be done on specimens sent by other laboratories in Switzerland within the surveillance program or by request of the cantonal physician team. Phylogenetic analysis data are produced by Nextstrain, in collaboration with Richard Neher’s group at the University of Basel and analyzed by Emma Hodcroft, from the Geneva Center of Emerging Viral Diseases and University of Geneva. In addition, partial Sanger sequencing may be done by our laboratory.

Geographic distribution, transmission advantage estimates and detailed numbers of available sequences over time in the canton of Geneva are available on the covSPECTRUM platform, run by Tanja Stadler’s group at ETH Zurich.

These reports are produced in collaboration with the Geneva Cantonal Physician team, which provides information on epidemiological links. For epidemiological data, please refer to the report of the cantonal physician team.